

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: HASTINGS, ET AL.

(ii) TITLE OF INVENTION: Human Vascular IBP-Like Growth Factor

(iii) NUMBER OF SEQUENCES: 8

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
CECCHI, STEWART & OLSTEIN

(B) STREET: 6 BECKER FARM ROAD

(C) CITY: ROSELAND

(D) STATE: NEW JERSEY

(E) COUNTRY: USA

(F) ZIP: 07068

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5 INCH DISKETTE

(B) COMPUTER: IBM PS/2

(C) OPERATING SYSTEM: MS-DOS

(D) SOFTWARE: WORD PERFECT 5.1

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE: Concurrently

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA

(A) APPLICATION NUMBER: PCT/US94/14388

(B) FILING DATE: 9 DEC 1994

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: FERRARO, GREGORY D.
- (B) REGISTRATION NUMBER: 36,134
- (C) REFERENCE/DOCKET NUMBER: 325800-332

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 201-994-1700
- (B) TELEFAX: 201-994-1744

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 1271 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTGCTTCCCA CCAGCAAAGA CCACGACTGG AGAGCCGAGC CGGAGCAGCT GGGAAACATG 60
AAGAGCGTCT TGCTGCTGAC CACGCTCCTC GTGCCTGCAC ACCTGGTGGC CGCCTGGAGC 120
AATAATTATG CGGTGGACTG CCCTCAACAC TGTGACAGCA GTGAGTGCAA AAGCAGCCCG 180
CGCTGCAAGA GGACAGTGCT CGACGACTGT GGCTGCTGCC GAGTGTGCGC TGCAGGGCGG 240
GGAGAAAACIT GCTACCGCAC AGTCTCAGGC ATGGATGGCA TGAAGTGTGG CCCGGGGCTG 300
AGGTGTCAGC CTTCTAATGG GGAGGATCCT TTTGGTGAAG AGTTTGGTAT CTGCAAAGAC 360
TGTCCCTACG GCACCTTCGG GATGGATTGC AGAGAGACCT GCAACTGCCA GTCAGGCATC 420
TGTGACAGGG GGACGGAAA ATGCCTGAAA TTCCCCCTCT TCCAATATTC AGTAACCAAG 480
TCTTCCAACA GATTGTTTC TCTCACGGAG CATGACATGG CATCTGGAGA TGGCAATATT 540
GTGAGAGAAG AAGTTGTGAA AGAGAATGCT GCCGGGTCTC CCGTAATGAG GAAATGGTTA 600
AATCCACGCT GATCCCGCT GTGATTTCTG AGAGAAGGCT CTATTTCTG GAYGTTCAA 660
CACACAGCCA ACATTTAGG AACTTTCTAG ATTATAGCAT AAGGACATGT AATTTTGAA 720
GACCAAATGT GATGCATGGT GGATCCAGAA AACAAAAAGT AGGATACTTA CAATCCATAA 780
CATCCATATG ACTGAACACT TGTATGTGTT TGTTAAATAT TCGAATGCAT GTAGATTTGT 840
TAAATGTGTG TGTATAGTAA CACTGAAGAA CTAAAATGC AATTTAGGTA ATCTTACATG 900
GAGACAGGTC AACCAAAGAG GGAGCTAGGC AAAGCTGAAG ACCGCAGTGA GTCAAATTAG 960
TTCTTGACT TTGATGTACA TTAATGTTGG GATATGGAAT GAAGACTTAA GAGCAGGAGA 1020

AGATGGGAG GGGGTGGGAG TGGGAAATAA AATATTTAGC CCTTCCTTGG TAGGTAGCTT 1080
CTCTAGAATT TAATTTTGCT TTTTTTTTTT TTTTTGGGCT TTGGGAAAG TCAAAATAAA 1140
ACAACCAGAA AACCCCTGAA GGAAGTAAGA TGTTTGAAGC TTATGGAAAT TTGAGTAACA 1200
AACAGCTTG ANCTGAGAGC AATTYCAAAA GGCTGCTGAT GTAGCCCCCG GGTTNCCTNT 1260
NTCTNAAGGA C 1271

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 184 AMINO ACIDS
- (B) TYPE: AMINO ACID
- (C) STRANDEDNESS:
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Lys Ser Val Leu Leu Leu Thr Thr Leu Leu Val Pro Ala His
-20 -15 -10
Leu Val Ala Ala Trp Ser Asn Asn Tyr Ala Val Asp Cys Pro Gln
-5 1 5
His Cys Asp Ser Ser Glu Cys Lys Ser Ser Pro Arg Cys Lys Arg
10 15 20
Thr Val Leu Asp Asp Cys Gly Cys Cys Arg Val Cys Ala Ala Gly
25 30 35
Arg Gly Glu Thr Cys Tyr Arg Thr Val Ser Gly Met Asp Gly Met
40 45 50
Lys Cys Gly Pro Gly Leu Arg Cys Gln Pro Ser Asn Gly Glu Asp
55 60 65
Pro Phe Gly Glu Glu Phe Gly Ile Cys Lys Asp Cys Pro Tyr Gly
70 75 80
Thr Phe Gly Met Asp Cys Arg Glu Thr Cys Asn Cys Gln Ser Gly
85 90 95
Ile Cys Asp Arg Gly Thr Gly Lys Cys Leu Lys Phe Pro Phe Phe
100 105 110

Gln Tyr Ser Val Thr Lys Ser Ser Asn Arg Phe Val Ser Leu Thr
115 120 125
Glu His Asp Met Ala Ser Gly Asp Gly Asn Ile Val Arg Glu Glu
130 135 140
Val Val Lys Glu Asn Ala Ala Gly Ser Pro Val Met Arg Lys Trp
145 150 155
Leu Asn Pro Arg
160